

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/735, 289
Source: JFWO
Date Processed by STIC: 11-19-04

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 11/19/2004

PATENT APPLICATION: US/10/735,289

TIME: 17:05:48

Input Set : A:\Sequence Listing.txt

Output Set: N:\CRF4\11192004\J735289.raw

4 <110> APPLICANT: Zhu, J.
 5 Ding, A.
 6 Nathan, C.
 8 <120> TITLE OF INVENTION: Use of proepithelin to promote wound
 9 repair and reduce inflammation
 11 <130> FILE REFERENCE: 1676.011US1
 13 <140> CURRENT APPLICATION NUMBER: US 10/735,289
 14 <141> CURRENT FILING DATE: 2003-12-12
 16 <150> PRIOR APPLICATION NUMBER: 60/432,948
 17 <151> PRIOR FILING DATE: 2002-12-12
 19 <160> NUMBER OF SEQ ID NOS: 32
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 593
 25 <212> TYPE: PRT
 26 <213> ORGANISM: Homo sapiens
 28 <400> SEQUENCE: 1
 29 Met Trp Thr Leu Val Ser Trp Val Ala Leu Thr Ala Gly Leu Val Ala
 30 1 5 10 15
 31 Gly Thr Arg Cys Pro Asp Gly Gln Phe Cys Pro Val Ala Cys Cys Leu
 32 20 25 30
 33 Asp Pro Gly Gly Ala Ser Tyr Ser Cys Cys Arg Pro Leu Leu Asp Lys
 34 35 40 45
 35 Trp Pro Thr Thr Leu Ser Arg His Leu Gly Gly Pro Cys Gln Val Asp
 36 50 55 60
 37 Ala His Cys Ser Ala Gly His Ser Cys Ile Phe Thr Val Ser Gly Thr
 38 65 70 75 80
 39 Ser Ser Cys Cys Pro Phe Pro Glu Ala Val Ala Cys Gly Asp Gly His
 40 85 90 95
 41 His Cys Cys Pro Arg Gly Phe His Cys Ser Ala Asp Gly Arg Ser Cys
 42 100 105 110
 43 Phe Gln Arg Ser Gly Asn Asn Ser Val Gly Ala Ile Gln Cys Pro Asp
 44 115 120 125
 45 Ser Gln Phe Glu Cys Pro Asp Phe Ser Thr Cys Cys Val Met Val Asp
 46 130 135 140
 47 Gly Ser Trp Gly Cys Cys Pro Met Pro Gln Ala Ser Cys Cys Glu Asp
 48 145 150 155 160
 49 Arg Val His Cys Cys Pro His Gly Ala Phe Cys Asp Leu Val His Thr
 50 165 170 175
 51 Arg Cys Ile Thr Pro Thr Gly Thr His Pro Leu Ala Lys Lys Leu Pro
 52 180 185 190
 53 Ala Gln Arg Thr Asn Arg Ala Val Ala Leu Ser Ser Ser Val Met Cys
 54 195 200 205

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55 Pro Asp Ala Arg Ser Arg Cys Pro Asp Gly Ser Thr Cys Cys Glu Leu
56      210                215                220
57 Pro Ser Gly Lys Tyr Gly Cys Cys Pro Met Pro Asn Ala Thr Cys Cys
58 225                230                235                240
59 Ser Asp His Leu His Cys Cys Pro Gln Asp Thr Val Cys Asp Leu Ile
60      245                250                255
61 Gln Ser Lys Cys Leu Ser Lys Glu Asn Ala Thr Thr Asp Leu Leu Thr
62      260                265                270
63 Lys Leu Pro Ala His Thr Val Gly Asp Val Lys Cys Asp Met Glu Val
64      275                280                285
65 Ser Cys Pro Asp Gly Tyr Thr Cys Cys Arg Leu Gln Ser Gly Ala Trp
66      290                295                300
67 Gly Cys Cys Pro Phe Thr Gln Ala Val Cys Cys Glu Asp His Ile His
68 305                310                315                320
69 Cys Cys Pro Ala Gly Phe Thr Cys Asp Thr Gln Lys Gly Thr Cys Glu
70      325                330                335
71 Gln Gly Pro His Gln Val Pro Trp Met Glu Lys Ala Pro Ala His Leu
72      340                345                350
73 Ser Leu Pro Asp Pro Gln Ala Leu Lys Arg Asp Val Pro Cys Asp Asn
74      355                360                365
75 Val Ser Ser Cys Pro Ser Ser Asp Thr Cys Cys Gln Leu Thr Ser Gly
76      370                375                380
77 Glu Trp Gly Cys Cys Pro Ile Pro Glu Ala Val Cys Cys Ser Asp His
78 385                390                395                400
79 Gln His Cys Cys Pro Gln Gly Tyr Thr Cys Val Ala Glu Gly Gln Cys
80      405                410                415
81 Gln Arg Gly Ser Glu Ile Val Ala Gly Leu Glu Lys Met Pro Ala Arg
82      420                425                430
83 Arg Ala Ser Leu Ser His Pro Arg Asp Ile Gly Cys Asp Gln His Thr
84      435                440                445
85 Ser Cys Pro Val Gly Gly Thr Cys Cys Pro Ser Leu Gly Gly Ser Trp
86      450                455                460
87 Ala Cys Cys Gln Leu Pro His Ala Val Cys Cys Glu Asp Arg Gln His
88 465                470                475                480
89 Cys Cys Pro Ala Gly Tyr Thr Cys Asn Val Lys Ala Arg Ser Cys Glu
90      485                490                495
91 Lys Glu Val Val Ser Ala Gln Pro Ala Thr Phe Leu Ala Arg Ser Pro
92      500                505                510
93 His Val Gly Val Lys Asp Val Glu Cys Gly Glu Gly His Phe Cys His
94      515                520                525
95 Asp Asn Gln Thr Cys Cys Arg Asp Asn Arg Gln Gly Trp Ala Cys Cys
96      530                535                540
97 Pro Tyr Arg Gln Gly Val Cys Cys Ala Asp Arg Arg His Cys Cys Pro
98 545                550                555                560
99 Ala Gly Phe Arg Cys Ala Ala Arg Gly Thr Lys Cys Leu Arg Arg Glu
100      565                570                575
101 Ala Pro Arg Trp Asp Ala Pro Leu Arg Asp Pro Ala Leu Arg Gln Leu
102      580                585                590
103 Leu

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107 <210> SEQ ID NO: 2
108 <211> LENGTH: 593
109 <212> TYPE: PRT
110 <213> ORGANISM: Homo sapiens
112 <400> SEQUENCE: 2
113 Met Trp Thr Leu Val Ser Trp Val Ala Leu Thr Ala Gly Leu Val Ala
114 1 5 10 15
115 Gly Thr Arg Cys Pro Asp Gly Gln Phe Cys Pro Val Ala Cys Cys Leu
116 20 25 30
117 Asp Pro Gly Gly Ala Ser Tyr Ser Cys Cys Arg Pro Leu Leu Asp Lys
118 35 40 45
119 Trp Pro Thr Thr Leu Ser Arg His Leu Gly Gly Pro Cys Gln Val Asp
120 50 55 60
121 Ala His Cys Ser Ala Gly His Ser Cys Ile Phe Thr Val Ser Gly Thr
122 65 70 75 80
123 Ser Ser Cys Cys Pro Phe Pro Glu Ala Val Ala Cys Gly Asp Gly His
124 85 90 95
125 His Cys Cys Pro Arg Gly Phe His Cys Ser Ala Asp Gly Arg Ser Cys
126 100 105 110
127 Phe Gln Arg Ser Gly Asn Asn Ser Val Gly Ala Ile Gln Cys Pro Asp
128 115 120 125
129 Ser Gln Phe Glu Cys Pro Asp Phe Ser Thr Cys Cys Val Met Val Asp
130 130 135 140
131 Gly Ser Trp Gly Cys Cys Pro Met Pro Gln Ala Ser Cys Cys Glu Asp
132 145 150 155 160
133 Arg Val His Cys Cys Pro His Gly Ala Phe Cys Asp Leu Val His Thr
134 165 170 175
135 Arg Cys Ile Thr Pro Thr Gly Thr His Pro Leu Ala Lys Lys Leu Pro
136 180 185 190
137 Ala Gln Arg Thr Asn Arg Ala Val Ala Leu Ser Ser Ser Val Met Cys
138 195 200 205
139 Pro Asp Ala Arg Ser Arg Cys Pro Asp Gly Ser Thr Cys Cys Glu Leu
140 210 215 220
141 Pro Ser Gly Lys Tyr Gly Cys Cys Pro Met Pro Asn Ala Thr Cys Cys
142 225 230 235 240
143 Ser Asp His Leu His Cys Cys Pro Gln Asp Thr Val Cys Asp Leu Ile
144 245 250 255
145 Gln Ser Lys Cys Leu Ser Lys Glu Asn Ala Thr Thr Asp Leu Leu Thr
146 260 265 270
147 Lys Leu Pro Ala His Thr Val Gly Asp Val Lys Cys Asp Met Glu Val
148 275 280 285
149 Ser Cys Pro Asp Gly Tyr Thr Cys Cys Arg Leu Gln Ser Gly Ala Trp
150 290 295 300
151 Gly Cys Cys Pro Phe Thr Gln Ala Val Cys Cys Glu Asp His Ile His
152 305 310 315 320
153 Cys Cys Pro Ala Gly Phe Thr Cys Asp Thr Gln Lys Gly Thr Cys Glu
154 325 330 335
155 Gln Gly Pro His Gln Val Pro Trp Met Glu Lys Ala Pro Ala His Leu
156 340 345 350

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157 Ser Leu Pro Asp Pro Gln Ala Leu Lys Arg Asp Val Pro Cys Asp Asn
158           355           360           365
159 Val Ser Ser Cys Pro Ser Ser Asp Thr Cys Cys Gln Leu Thr Ser Gly
160       370           375           380
161 Glu Trp Gly Cys Cys Pro Ile Pro Glu Ala Val Cys Cys Ser Asp His
162 385           390           395           400
163 Gln His Cys Cys Pro Gln Gly Tyr Thr Cys Val Ala Glu Gly Gln Cys
164           405           410           415
165 Gln Arg Gly Ser Glu Ile Val Ala Gly Leu Glu Lys Met Pro Ala Arg
166           420           425           430
167 Arg Ala Ser Leu Ser His Pro Arg Asp Ile Gly Cys Asp Gln His Thr
168           435           440           445
169 Ser Cys Pro Val Gly Gln Thr Cys Cys Pro Ser Leu Gly Gly Ser Trp
170       450           455           460
171 Ala Cys Cys Gln Leu Pro His Ala Val Cys Cys Glu Asp Arg Gln His
172 465           470           475           480
173 Cys Cys Pro Ala Gly Tyr Thr Cys Asn Val Lys Ala Arg Ser Cys Glu
174           485           490           495
175 Lys Glu Val Val Ser Ala Gln Pro Ala Thr Phe Leu Ala Arg Ser Pro
176           500           505           510
177 His Val Gly Val Lys Asp Val Glu Cys Gly Glu Gly His Phe Cys His
178           515           520           525
179 Asp Asn Gln Thr Cys Cys Arg Asp Asn Arg Gln Gly Trp Ala Cys Cys
180       530           535           540
181 Pro Tyr Arg Gln Gly Val Cys Cys Ala Asp Arg Arg His Cys Cys Pro
182 545           550           555           560
183 Ala Gly Phe Arg Cys Ala Ala Arg Gly Thr Lys Cys Leu Arg Arg Glu
184           565           570           575
185 Ala Pro Arg Trp Asp Ala Pro Leu Arg Asp Pro Ala Leu Arg Gln Leu
186       580           585           590
187 Leu
191 <210> SEQ ID NO: 3
192 <211> LENGTH: 2178
193 <212> TYPE: DNA
194 <213> ORGANISM: Homo sapiens
196 <400> SEQUENCE: 3
197 gtagtctgag cgctaccggg ttgctgctgc ccaaggaccg cggagtcgga cgcaggcaga 60
198 ccatgtggac cctggtgagc tgggtggcct taacagcagg gctggtggct ggaacgcggt 120
199 gccagatgg tcagtctgc cctgtggcct gctgacctga ccccgaggga gccagctaca 180
200 gctgctgccc tcccctctg gacaaatggc ccacaacact gagcaggcat ctgggtggcc 240
201 cctgccaggt tgatgccac tgctctgccc gccactcctg catcttacc gtctcaggga 300
202 cttccagttg ctgcccttc ccagaggccg tggcatgcgg ggatggccat cactgctgcc 360
203 cacggggcct ccactgcagt gcagacgggc gatcctgctt ccaaatatca ggtaacaact 420
204 cgtgggtgac catcagtgct cctgatagtc agttcgaatg cccggacttc tccacgtgct 480
205 gtgttatggt cgtgtgctcc tgggggtgct gccccatgcc ccaggcttcc tgctgtgaag 540
206 acaggggtgca ctgctgtccc cacgggtgect tctgacacct gggtcacacc cgctgcatca 600
207 caccacaggg caccacccc ctggcaaga agctcctgct ccagaggact aacagggcag 660
208 tggccttgct cagctcggtc atgtgtccgg acgcacggtc cgggtgcct gatggttcta 720
209 cctgctgtga gctgcccagt ggaagtatg gctgctgccc aatgccaac gccacctgct 780

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210 gctccgatca cctgcaactgc tgcccccaag acaactgtgtg tgacctgac cagagtaagt 840
211 gcctctccaa ggagaacgct accacggacc tcctcactaa gctgcctgcg cacacagtgg 900
212 gggatgtgaa atgtgacatg gaggtgagct gccagatgg ctataactgc tgccgtctac 960
213 agtcgggggc ctggggctgc tgccctttta cccaggctgt gtgctgtgag gaccacatac 1020
214 actgctgtcc cgcggggttt acgtgtgaca cgcagaaggg tacctgtgaa caggggcccc 1080
215 accaggtgcc ctggatggag aaggccccag ctacactcag cctgccagac ccacaagcct 1140
216 tgaagagaga tgtccctgt gataatgtca gcagctgtcc ctccctcgat acctgctgcc 1200
217 aactcacgtc tggggagtgg ggctgctgtc caatcccaga ggctgtctgc tgcteggacc 1260
218 accagcaactg ctgccccag ggctacacgt gtgtagctga ggggcagtgt cagcgaggaa 1320
219 gcgagatcgt ggctggactg gagaagatgc ctgcccgcgc ggcttcctta tcccacccca 1380
220 gagacatcgg ctgtgaccag cacaccagct gcccggtggg gcagacctgc tgcccagacc 1440
221 tgggtgggag ctgggctgc tgccagttgc cccatgctgt gtgctgcgag gatcgccagc 1500
222 actgctgccc ggctggctac acctgcaacg tgaaggctcg atcctgcgag aaggaagtgg 1560
223 tctctgcccc gcctgccacc tcctggccc gttagcctca cgtgggtgtg aaggactgg 1620
224 agtgtgggga aggacacttc tgccatgata accagacctg ctgccgagac aaccgacagg 1680
225 gctgggctg ctgtccctac cgcacgggag tctgtgtgct tgatcggcgc cactgctgtc 1740
226 ctgctggctt ccgctgcgca gccaggggta ccaagtgtt gcgcaggag gccccgcgct 1800
227 gggacgcccc tttgagggac ccagccttga gacagctgct gtgagggaca gtactgaaga 1860
228 ctctgcagcc ctcgggacc cactcgagg gtgcccctc ctcaggcctc cctagcacct 1920
229 ccccctaacc aaattctccc tggacccat tctgagctcc ccatcaccat gggaggtggg 1980
230 gcctcaatct aaggccttcc ctgtcagaag ggggtgtgg caaaagccac attacaagct 2040
231 gccatccctt ccccgtttca gtggaccctg tggccaggtg cttttcccta tccacagggg 2100
232 tgtttgtgtg tgtgcgcgtg tgcgtttcaa taaagttgt acactttcaa aaaaaaaaaa 2160
233 aaaaaaaaaa aaaaaaaaaa 2178

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236 <210> SEQ ID NO: 4

237 <211> LENGTH: 589

238 <212> TYPE: PRT

239 <213> ORGANISM: Mus musculus

241 <400> SEQUENCE: 4

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242 Met Trp Val Leu Met Ser Trp Leu Ala Phe Ala Ala Gly Leu Val Ala
243 1 5 10 15
244 Gly Thr Gln Cys Pro Asp Gly Gln Phe Cys Pro Val Ala Cys Cys Leu
245 20 25 30
246 Asp Gln Gly Gly Ala Asn Tyr Ser Cys Cys Asn Pro Leu Leu Asp Thr
247 35 40 45
248 Trp Pro Arg Ile Thr Ser His His Leu Asp Gly Ser Cys Gln Thr His
249 50 55 60
250 Gly His Cys Pro Ala Gly Tyr Ser Cys Leu Leu Thr Val Ser Gly Thr
251 65 70 75 80
252 Ser Ser Cys Cys Pro Phe Ser Lys Gly Val Ser Cys Gly Asp Gly Tyr
253 85 90 95
254 His Cys Cys Pro Gln Gly Phe His Cys Ser Ala Asp Gly Lys Ser Cys
255 100 105 110
256 Phe Gln Met Ser Asp Asn Pro Leu Gly Ala Val Gln Cys Pro Gly Ser
257 115 120 125
258 Gln Phe Glu Cys Pro Asp Ser Ala Thr Cys Cys Ile Met Val Asp Gly
259 130 135 140
260 Ser Trp Gly Cys Cys Pro Met Pro Gln Ala Ser Cys Cys Glu Asp Arg
261 145 150 155 160

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VERIFICATION SUMMARY

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